



#12/

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SEQUENCE LISTING

<110> SIEMEISTER, GERHARD
HABEREY, MARTIN
THIERAUCH, KARL-HEINZ

<120> COMBINATIONS AND COMPOSITIONS WHICH INTERFERE WITH
VEGF/VEGF AND ANGIOPOIETIN/TIE RECEPTOR FUNCTION
AND THEIR USE

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<140> 09/887,527

<141> 2001-06-25

<150> DE 00250194.8

<151> 2000-06-23

<150> DE 00250214.4

<151> 2000-06-28

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<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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<211> 2041

<212> DNA

<213> Homo sapiens

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<211> 235

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18

<211> 2732

<212> DNA

<213> Homo sapiens

<400> 18

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<213> Homo sapiens

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<211> 2361

<212> DNA

<213> Homo sapiens

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<210> 25

<211> 1420

<212> DNA

<213> Homo sapiens

<400> 25

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<210> 26

<211> 689

<212> DNA

<213> Homo sapiens

<400> 26

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<210> 27

<211> 471

<212> DNA

<213> Homo sapiens

<400> 27

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tgggcaattt ttgtatccaa ggaaataatg tgaatgcgag gaaatgtctt tagagcacag 420

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ggacagaggg ggaaataaga ggaggagaaa gctctctata ccaaagactg a 471

<210> 28

<211> 929

<212> DNA

<213> Homo sapiens

<400> 28

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<210> 29

<211> 1775

<212> DNA

<213> Homo sapiens

<400> 29

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<210> 30

<211> 1546

<212> DNA

<213> Homo sapiens

<400> 30

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ccaacaactg gaacaactcc taaaggaaca atcaccaatg aattacttaa aatgtctctg 360
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<210> 31

<211> 750

<212> DNA

<213> Homo sapiens

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<210> 32
 <211> 1620
 <212> DNA
 <213> Homo sapiens

<400> 32

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<210> 33
 <211> 2968
 <212> DNA
 <213> Homo sapiens

<400> 33

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<210> 34

<211> 6011

<212> DNA

<213> Homo sapiens

<400> 34

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<212> DNA

<213> Homo sapiens

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<211> 987

<212> DNA

<213> Homo sapiens

<400> 41

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<211> 956

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 1630

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<211> 921

<212> DNA

<213> Homo sapiens

<400> 49

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<213> Homo sapiens

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<211> 1191

<212> DNA

<213> Homo sapiens

<400> 51

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<211> 1200

<212> DNA

<213> Homo sapiens

<400> 52

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<212> DNA

<213> Homo sapiens

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<211> 250

<212> DNA

<213> Homo sapiens

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<211> 2270

<212> DNA

<213> Homo sapiens

<400> 55

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<210> 56

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 56

```

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cagtttgatt ggaagtccag ctgtgaaacc tggagcgctg ccttctcccc agatggctcc 180
tggtttgctt ggtctcaagg acactgcac gtcaaactga tcccctggcc gttggaggag 240
cagttcatcc cttaaagggtt tgaagccaaa agccgaagta gcaaaaatga gacgaaaggg 300
cggggcagcc caaaagagaa gacgctggac tgtggtcaga ttgtctgggg gctggccttc 360
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aagacaattt gatacataat aaaaaattat gacaatgtcc tgggaaaaaa aaaatgtaga 1560
aagatggtga agggtgggat ggatgaggag cgtggtgacg ggggcctgca gcgggttggg 1620
gaccctgtgc tgcgtt                                     1636

```

<210> 57

<211> 460

<212> DNA

<213> Homo sapiens

<400> 57

```

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tggaatgagc taaagcagcc gcctgggggtg ggaggccgag cccatttgta tgcagcaggg 180
ggcagcagcc cagcaaggga gcctccattc ccaggactct ggagggagct gagaccatcc 240
atgcccgcag agccctccct cacactccat cctgtccagc cctaattgtg caggtgggga 300
aactgagggt gggaaagtcac atagcaagtg actggcagag ctgggactgg aacccaacca 360
gcctcctaga ccacggttct tcccatcaat ggaatgctag agactccagc caggtgggta 420
ccgagctcga attcgtaatc atggtcatag ctgtttcctg                                     460

```

<210> 58

<211> 1049

<212> DNA

<213> Homo sapiens

<400> 58

```

atctgatcaa gaatacctgc cctggtcact ctgcggatgt ttctgtccac ttgttcacat 60
tgaggaccaaa gatatccttt tttacagagg cacttgctcg gtctaacaca gacacctcca 120
tgacgacatg ctggctcaca ttttgaggtt ctgcagaagt cccctcccca gcctggacta 180
cagcagcact ttcccgtggg ggtgcagtag ccgtttcgac agagcctgga gcaactctgaa 240
gtcagtgtct gtgcagggtt taccgtggct ctgcattcct caggcattaa aggtcttttg 300
ggatctacaaa ttttgtagag ttttccattg tgagtctggg tcatactttt actgcttgat 360
aaaatgtaaa cttcacctag ttcattctt ccaaatccca agatgtgacc ggaaaagtag 420

```

```

cctctacagg acccactagt gccgacacag agtgggttttt cttgccactg ctttgtcaca 480
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aatctttctg actggcagcc ccggtataca aatccacca ccaaaggacc attactgaat 600
ggcttgaatt ctaaaagtga tggctcactt tcataatctt tcccctttat tatctgtaga 660
attctggctg atgatctgtt ttttccattg gagtctgaac acagtatcgt taaattgatg 720
tttatatcag tgggatgtct atccacagca catctgcctg gatcgtggag cccatgagca 780
aacacttcgg ggggctgggt ggtgctgttg aagtgtgggt tgctccttgg tatggaataa 840
ggcaggttgc acatgtctgt gtccacatcc agccgtagca ctgagcctgt gaaatcactt 900
aaccatcca tttcttccat atcatccagt gtaatcatcc catcaccaag aatgatgtac 960
aaaaaccgct cagggccaaa gagcagttgc cctcccagat gctttctgtg gagttctgca 1020
acttcaagaa agactctggc tggtctcaa                                1049

```

<210> 59

<211> 747

<212> DNA

<213> Homo sapiens

<400> 59

```

tttttcaaat cacatatggc ttctttgacc ccatcaaata actttattca cacaaacgtc 60
ccttaattta caaagcctca gtcattcata cacattaggg gatccacagt gttcaaggaa 120
cttaaatata atgtatcata ccaaccctaa taaaccaagt acaaaaaata ttcatataaa 180
gttgttcaca cgtaggtcct agattaccag cttctgtgca aaaaaaggaa atgaagaaaa 240
atagatttat taactagtat tggaaactaa ctttgtgcct ggcttaaaac ctccctcacg 300
ctcgtctgtc ccacacaaat gtttaagaag tcaactgcaat gtactccccg gctctgatga 360
aaagaagccc ctggcacaaa agattccagt gccctgaag aggcctccctt cctcctgtgg 420
gctctcctag aaaaccagcg ggacggcctc cctgctgata ccgtctataa ccttaggggg 480
ccctcgggca ggcaacggca gtggactcat ctcggtgatg gctgtagatg ctaacactgg 540
ccaattcaat gccacaccta ctggttacct tttgagggca tttctccaga cagaagcccc 600
ttgaagccta ggtagggcag gatcagagat acaccgctgt ttgtctcgaa gggctccaca 660
gccagtagcg acatgcttgc agaagtagta tctctggact tctgcctcca gtcgaccggc 720
cgcgaaatata gtagtaatat cggccgcg                                747

```

<210> 60

<211> 1036

<212> PRT

<213> Homo sapiens

<400> 60

```

Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu
  1              5              10              15

```

```

Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Pro Ala Arg Ser Gly Thr
      20              25              30

```

```

Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
      35              40              45

```

```

Arg Asn Arg Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
      50              55              60

```

```

Thr Cys Ala Ser Gln Gly Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
      65              70              75              80

```

```

Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
      85              90              95

```

Asn	Gly	Asp	Ser	Leu	Thr	Glu	Tyr	Glu	Ala	Gly	Val	Cys	Glu	Asp	Glu	
			100					105					110			
Asn	Trp	Thr	Asp	Asp	Gln	Leu	Leu	Gly	Phe	Lys	Pro	Cys	Asn	Glu	Asn	
		115					120					125				
Leu	Ile	Ala	Gly	Cys	Asn	Ile	Ile	Asn	Gly	Lys	Cys	Glu	Cys	Asn	Thr	
	130					135					140					
Ile	Arg	Thr	Cys	Ser	Asn	Pro	Phe	Glu	Phe	Pro	Ser	Gln	Asp	Met	Cys	
145					150					155					160	
Leu	Ser	Ala	Leu	Lys	Arg	Ile	Glu	Glu	Glu	Lys	Pro	Asp	Cys	Ser	Lys	
				165					170					175		
Ala	Arg	Cys	Glu	Val	Gln	Phe	Ser	Pro	Arg	Cys	Pro	Glu	Asp	Ser	Val	
			180					185					190			
Leu	Ile	Glu	Gly	Tyr	Ala	Pro	Pro	Gly	Glu	Cys	Cys	Pro	Leu	Pro	Ser	
	195					200						205				
Arg	Cys	Val	Cys	Asn	Pro	Ala	Gly	Cys	Leu	Arg	Lys	Val	Cys	Gln	Pro	
	210					215					220					
Gly	Asn	Leu	Asn	Ile	Leu	Val	Ser	Lys	Ala	Ser	Gly	Lys	Pro	Gly	Glu	
225					230					235					240	
Cys	Cys	Asp	Leu	Tyr	Glu	Cys	Lys	Pro	Val	Phe	Gly	Val	Asp	Cys	Arg	
				245					250					255		
Thr	Val	Glu	Cys	Pro	Thr	Val	Gln	Gln	Thr	Ala	Cys	Pro	Pro	Asp	Ser	
			260					265						270		
Tyr	Glu	Thr	Gln	Val	Arg	Leu	Thr	Ala	Asp	Gly	Cys	Cys	Thr	Leu	Pro	
	275						280					285				
Thr	Arg	Cys	Glu	Cys	Leu	Ser	Gly	Leu	Cys	Gly	Phe	Pro	Val	Cys	Glu	
	290					295					300					
Val	Gly	Ser	Thr	Pro	Arg	Ile	Val	Ser	Arg	Gly	Asp	Gly	Thr	Pro	Gly	
305					310					315					320	
Lys	Cys	Cys	Asp	Val	Phe	Glu	Cys	Val	Asn	Asp	Thr	Lys	Pro	Ala	Cys	
				325					330					335		
Val	Phe	Asn	Asn	Val	Glu	Tyr	Tyr	Asp	Gly	Asp	Met	Phe	Arg	Met	Asp	
			340					345					350			
Asn	Cys	Arg	Phe	Cys	Arg	Cys	Gln	Gly	Gly	Val	Ala	Ile	Cys	Phe	Thr	
	355						360					365				
Ala	Gln	Cys	Gly	Glu	Ile	Asn	Cys	Glu	Arg	Tyr	Tyr	Val	Pro	Glu	Gly	
	370					375					380					
Glu	Cys	Cys	Pro	Val	Cys	Glu	Asp	Pro	Val	Tyr	Pro	Phe	Asn	Asn	Pro	
385					390					395					400	

Ala Gly Cys Tyr Ala Asn Gly Leu Ile Leu Ala His Gly Asp Arg Trp
 405 410 415
 Arg Glu Asp Asp Cys Thr Phe Cys Gln Cys Val Asn Gly Glu Arg His
 420 425 430
 Cys Val Ala Thr Val Cys Gly Gln Thr Cys Thr Asn Pro Val Lys Val
 435 440 445
 Pro Gly Glu Cys Cys Pro Val Cys Glu Glu Pro Thr Ile Ile Thr Val
 450 455 460
 Asp Pro Pro Ala Cys Gly Glu Leu Ser Asn Cys Thr Leu Thr Arg Lys
 465 470 475 480
 Asp Cys Ile Asn Gly Phe Lys Arg Asp His Asn Gly Cys Arg Thr Cys
 485 490 495
 Gln Cys Ile Asn Thr Gln Glu Leu Cys Ser Glu Arg Lys Gln Gly Cys
 500 505 510
 Thr Leu Asn Cys Pro Phe Gly Phe Leu Thr Asp Ala Gln Asn Cys Glu
 515 520 525
 Ile Cys Glu Cys Arg Pro Arg Pro Lys Lys Cys Arg Pro Ile Ile Cys
 530 535 540
 Asp Lys Tyr Cys Pro Leu Gly Leu Leu Lys Asn Lys His Gly Cys Asp
 545 550 555 560
 Ile Cys Arg Cys Lys Lys Cys Pro Glu Leu Ser Cys Ser Lys Ile Cys
 565 570 575
 Pro Leu Gly Phe Gln Gln Asp Ser His Gly Cys Leu Ile Cys Lys Cys
 580 585 590
 Arg Glu Ala Ser Ala Ser Ala Gly Pro Pro Ile Leu Ser Gly Thr Cys
 595 600 605
 Leu Thr Val Asp Gly His His His Lys Asn Glu Glu Ser Trp His Asp
 610 615 620
 Gly Cys Arg Glu Cys Tyr Cys Leu Asn Gly Arg Glu Met Cys Ala Leu
 625 630 635 640
 Ile Thr Cys Pro Val Pro Ala Cys Gly Asn Pro Thr Ile His Pro Gly
 645 650 655
 Gln Cys Cys Pro Ser Cys Ala Asp Asp Phe Val Val Gln Lys Pro Glu
 660 665 670
 Leu Ser Thr Pro Ser Ile Cys His Ala Pro Gly Gly Glu Tyr Phe Val
 675 680 685
 Glu Gly Glu Thr Trp Asn Ile Asp Ser Cys Thr Gln Cys Thr Cys His
 690 695 700

Ser Gly Arg Val Leu Cys Glu Thr Glu Val Cys Pro Pro Leu Leu Cys
 705 710 715 720
 Gln Asn Pro Ser Arg Thr Gln Asp Ser Cys Cys Pro Gln Cys Thr Asp
 725 730 735
 Gln Pro Phe Arg Pro Ser Leu Ser Arg Asn Asn Ser Val Pro Asn Tyr
 740 745 750
 Cys Lys Asn Asp Glu Gly Asp Ile Phe Leu Ala Ala Glu Ser Trp Lys
 755 760 765
 Pro Asp Val Cys Thr Ser Cys Ile Cys Ile Asp Ser Val Ile Ser Cys
 770 775 780
 Phe Ser Glu Ser Cys Pro Ser Val Ser Cys Glu Arg Pro Val Leu Arg
 785 790 795 800
 Lys Gly Gln Cys Cys Pro Tyr Cys Ile Lys Asp Thr Ile Pro Lys Lys
 805 810 815
 Val Val Cys His Phe Ser Gly Lys Ala Tyr Ala Asp Glu Glu Arg Trp
 820 825 830
 Asp Leu Asp Ser Cys Thr His Cys Tyr Cys Leu Gln Gly Gln Thr Leu
 835 840 845
 Cys Ser Thr Val Ser Cys Pro Pro Leu Pro Cys Val Glu Pro Ile Asn
 850 855 860
 Val Glu Gly Ser Cys Cys Pro Met Cys Pro Glu Met Tyr Val Pro Glu
 865 870 875 880
 Pro Thr Asn Ile Pro Ile Glu Lys Thr Asn His Arg Gly Glu Val Asp
 885 890 895
 Leu Glu Val Pro Leu Trp Pro Thr Pro Ser Glu Asn Asp Ile Val His
 900 905 910
 Leu Pro Arg Asp Met Gly His Leu Gln Val Asp Tyr Arg Asp Asn Arg
 915 920 925
 Leu His Pro Ser Glu Asp Ser Ser Leu Asp Ser Ile Ala Ser Val Val
 930 935 940
 Val Pro Ile Ile Ile Cys Leu Ser Ile Ile Ile Ala Phe Leu Phe Ile
 945 950 955 960
 Asn Gln Lys Lys Gln Trp Ile Pro Leu Leu Cys Trp Tyr Arg Thr Pro
 965 970 975
 Thr Lys Pro Ser Ser Leu Asn Asn Gln Leu Val Ser Val Asp Cys Lys
 980 985 990
 Lys Gly Thr Arg Val Gln Val Asp Ser Ser Gln Arg Met Leu Arg Ile
 995 1000 1005

Ala Glu Pro Asp Ala Arg Phe Ser Gly Phe Tyr Ser Met Gln Lys Gln
1010 1015 1020

Asn His Leu Gln Ala Asp Asn Phe Tyr Gln Thr Val
1025 1030 1035